

Spacer	22%
Sixth EGF repeat	40%
"99aa spacer"	38%
Seventh EGF repeat	11% /NA
Eighth EGF repeat	44%
Nineth EGF repeat	29% /NA
Cysteine knot motif	34%

NA: not applicable due to absence of homologous repeat.

Figures for individual LLRs are shown in brackets.--

*See
a 3*
Immediately prior to the claims, please insert the enclosed 23 page section entitled
'SEQUENCE LISTING'.

Please delete all pages after page 17.

IN THE CLAIMS

Please cancel all pending claims (1-7) and add new claims 8-27 as follows:

8. (New) A mixture comprising an isolated Slit polypeptide and a Robo polypeptide, said Slit polypeptide comprising at least one sequence selected from the group consisting of SEQ ID NOS:2-14, or a subsequence thereof having at least 16 consecutive amino acid residues thereof.

8. (New) A mixture according to claim *8*, the ¹ *first* Slit polypeptide comprising at least one sequence selected from the group consisting of SEQ ID NOS:2-14, or a subsequence thereof having at least 64 consecutive amino acid residues thereof.

9. (New) A mixture according to claim *8*, the ¹ *first* Slit polypeptide comprising at least one sequence selected from the group consisting of SEQ ID NOS:2-14.

4. (New) A mixture according to claim *8*, the ¹ *first* Slit polypeptide comprising SEQ ID NO:2, or a subsequence thereof having at least 16 consecutive amino acid residues thereof.

5. (New) A mixture according to claim *8*, the ¹ *first* Slit polypeptide comprising SEQ ID NO:2, or a subsequence thereof having at least 64 consecutive amino acid residues thereof.

6. (New) A mixture according to claim *8*, the *Slit* polypeptide comprising at least one sequence selected from the group consisting of SEQ ID NOS:3-6, or a subsequence thereof having at least 16 consecutive amino acid residues thereof.

7. (New) A mixture according to claim *8*, the *Slit* polypeptide comprising at least one sequence selected from the group consisting of SEQ ID NOS:3-6, or a subsequence thereof having at least 64 consecutive amino acid residues thereof.

8. (New) A mixture according to claim *8*, the *Slit* polypeptide comprising SEQ ID NO:7, or a subsequence thereof having at least 16 consecutive amino acid residues thereof.

9. (New) A mixture according to claim *8*, the *Slit* polypeptide comprising SEQ ID NO:7, or a subsequence thereof having at least 64 consecutive amino acid residues thereof.

10. (New) A mixture according to claim *8*, the *Slit* polypeptide comprising at least one sequence selected from the group consisting of SEQ ID NOS:8-9, or a subsequence thereof having at least 16 consecutive amino acid residues thereof.

11. (New) A mixture according to claim *8*, the *Slit* polypeptide comprising at least one sequence selected from the group consisting of SEQ ID NOS:8-9, or a subsequence thereof having at least 64 consecutive amino acid residues thereof.

12. (New) A mixture according to claim *8*, the *Slit* polypeptide comprising at least one sequence selected from the group consisting of SEQ ID NOS:10-11, or a subsequence thereof having at least 16 consecutive amino acid residues thereof.

13. (New) A mixture according to claim *8*, the *Slit* polypeptide comprising at least one sequence selected from the group consisting of SEQ ID NOS:10-11, or a subsequence thereof having at least 64 consecutive amino acid residues thereof.

14. (New) A mixture according to claim *8*, the *Slit* polypeptide comprising at least one sequence selected from the group consisting of SEQ ID NOS:12-14, or a subsequence thereof having at least 16 consecutive amino acid residues thereof.

5.
22. (New) A mixture according to claim 8, the ~~Slit~~ polypeptide comprising at least one sequence selected from the group consisting of SEQ ID NOS:12-14, or a subsequence thereof having at least 64 consecutive amino acid residues thereof.

16.
23. (New) A mixture according to claim 8, the ~~Slit~~ *first* polypeptide comprising at least one sequence selected from the group consisting of SEQ ID NO:2, amino acid residues 1-10; SEQ ID NO:2, amino acid residues 29-41; SEQ ID NO:2, amino acid residues 75-87; SEQ ID NO:2, amino acid residues 92-109; SEQ ID NO:2, amino acid residues 132-141; SEQ ID NO:2, amino acid residues 192-205; SEQ ID NO:2, amino acid residues 258-269; SEQ ID NO:2, amino acid residues 295-311; SEQ ID NO:2, amino acid residues 316-330; SEQ ID NO:2, amino acid residues 373-382; SEQ ID NO:2, amino acid residues 403-422; SEQ ID NO:2, amino acid residues 474-485; SEQ ID NO:2, amino acid residues 561-576; SEQ ID NO:2, amino acid residues 683-697; SEQ ID NO:2, amino acid residues 768-777; SEQ ID NO:2, amino acid residues 798-813; SEQ ID NO:2, amino acid residues 882-894; SEQ ID NO:2, amino acid residues 934-946; SEQ ID NO:2, amino acid residues 1054-1067; SEQ ID NO:2, amino acid residues 1181-1192; SEQ ID NO:2, amino acid residues 1273-1299; SEQ ID NO:2, amino acid residues 1383-1397; SEQ ID NO:2, amino acid residues 1468-1477; and SEQ ID NO:2, amino acid residues 1508-1517.

17.
24. (New) A mixture according to claim 8, comprising a cell comprising the ~~Robo~~ *Second* polypeptide.

25 18.
24. (New) A mixture according to claim 10, comprising a cell comprising the ~~Robo~~ *Second* polypeptide.

26 19.
25. (New) A mixture according to claim 8, comprising a candidate agent for modulating an interaction of the Robo and Slit polypeptides.

26.
26. (New) A method of identifying agents which modulate the interaction of a ~~Robo~~ *Second* polypeptide and a Slit polypeptide, said method comprising the steps of:
combining the mixture of claim 8 and a candidate agent under conditions whereby, but for the presence of the agent, the ~~Robo~~ *Second* and Slit *first* polypeptides engage in a first interaction, and determining a second interaction of the ~~Robo~~ *Second* and Slit *first* polypeptides in the presence of the agent,